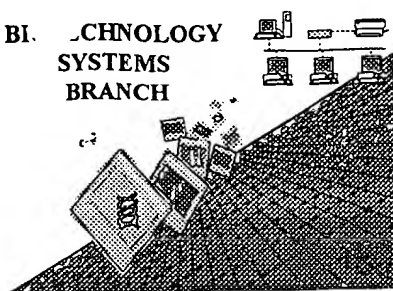


**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BI. TECHNOLOGY  
SYSTEMS  
BRANCH



16C1  
**RECEIVED**

NOV 13 2001

SCIENTIFIC AND TECHNICAL INFORMATION CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/441,242

Source: OIP

Date Processed by STIC: 7/26/2001

#12

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## RAW SEQUENCE LISTING

DATE: 07/26/2001

PATENT APPLICATION: US/09/441,242

TIME: 15:22:26

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

163 <210> SEQ ID NO: 4  
 164 <211> LENGTH: 108  
 165 <212> TYPE: PRT  
 166 <213> ORGANISM: Artificial  
 168 <220> FEATURE:  
 169 <223> OTHER INFORMATION: MTCPl protein  
 171 <220> FEATURE:  
 172 <221> NAME/KEY: site  
 173 <222> LOCATION: (1)..(108)  
 174 <223> OTHER INFORMATION: Xaa = any amino acid  
 177 <400> SEQUENCE: 4  
 179 Met Ala Gly Glu Asp Val Gly Ala Pro Pro Asp His Leu Trp Val His  
 180 1 5 10 15  
 182 Gln Glu Gly Ile Tyr Arg Asp Glu Tyr Gln Arg Thr Trp Val Ala Val  
 183 20 25 30  
 185 Val Glu Glu Glu Thr Ser Phe Leu Arg Ala Arg Val Gln Gln Ile Gln  
 186 35 40 45  
 188 Val Pro Leu Gly Asp Ala Ala Arg Pro Ser His Leu Leu Thr Ser Gln  
 189 50 55 60  
 191 Leu Pro Leu Met Trp Gln Leu Tyr Pro Glu Glu Arg Tyr Met Asp Asn  
 192 65 70 75 80  
 194 Asn Ser Arg Leu Trp Gln Ile Gln His His Leu Met Val Arg Gly Val  
 195 85 90 95  
 197 Gln Glu Leu Leu Leu Lys Leu Leu Pro Asp Asp Xaa  
 198 100 105  
 200 <210> SEQ ID NO: 5  
 201 <211> LENGTH: 4922  
 202 <212> TYPE: DNA  
 203 <213> ORGANISM: Artificial  
 205 <220> FEATURE:  
 206 <223> OTHER INFORMATION: genomic DNA of TCL-1  
 208 <220> FEATURE:  
 209 <221> NAME/KEY: modified\_base  
 210 <222> LOCATION: (1)..(4922)  
 211 <223> OTHER INFORMATION: m = a or c  
 212 r = a or g  
 213 w = a or t  
 214 s = c or g  
 217 <220> FEATURE:  
 218 <221> NAME/KEY: modified\_base  
 219 <222> LOCATION: (1)..(4922)  
 220 <223> OTHER INFORMATION: y = c or t  
 221 k = g or t  
 222 v = a, c or g  
 223 h = a, c or t  
 226 <220> FEATURE:  
 227 <221> NAME/KEY: modified\_base  
 228 <222> LOCATION: (1)..(4922)  
 229 <223> OTHER INFORMATION: d = a, g or t

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001

TIME: 15:22:26

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

```

230      b = c, g, or t
231      n = a, c, g, or t
234 <400> SEQUENCE: 5
235 gtcgacttgt gakttyccmag magaggccca gaagtcccg tccggcaaaag cggaggggaa      60
237 gcgggggggg tcttccaaga agaagaaagg gcccaagggt caacccccgg tgctttctcc      120
239 agcagcaagc aagaggggcg cgggtcggtt gtcgctgctg gccgggggcc tccaggagaa      180
241 ggcgcggroc agctggggcc ggggtctgctg tcccaggagc tgccaccggt ccaggagagca      240
243 agtcaggccg ggacgttagc gcctgcgcgg gacctcact tgccaccaag rmccccacaa      300
245 accccgcccc atcctgyctt acgccccgcc ccaaggctcg ttctccccga cccgggggtc      360
W--> 247 cccgccccaa ggnccgtcct ccccgccccc gccgsttggg ggcggccgca tgctgcccgg      420
249 atataaaggg tcggccccac atcccaggga ccagcgagcg gccttgagag gctctggctc      480
251 ttgctttctta ggcgccccga ggaagccatg gccgagtgcc cgacactcgg ggaggcagtc      540
253 accgaccacc cggaccgcct gtgggccttg gagaagttcg tgtatttgga cgagaagcag      600
255 macgcctgcc tgcccttaac catcgaggta caaccacct tggagcggat ggcgargcag      660
W--> 257 cagggggcasc ccctggggagc ttgggatncc ctaggaaggg cgaggactca aggagcactc      720
259 actatggggc agggaggatc ccccacagat kaagccactt ttggagccgg sctctkgagg      780
261 gatgaatagg agttcctoca ggcagggaag aagggtggga aaaccccaaa ggaatgtcgg      840
263 tcaaaggggt ggaccagtg cctgtggagt gtgactataa tgttgactac agcaggcatt      900
265 ttctgggctt cggggtccta atccttaaaa atgggtatct ctaagtgact catccatatg      960
267 gccgattatc ggaatcatct cagggtgggtc ccagaaatct gtatttttaa aaagaaccow      1020
269 cmacagttta ggggtccaacc caggcataac caaaacactg gcctaagagt tgtgaagtat      1080
271 tttcccacct accctctggg ctttatttaa gamaaccaa tttacaagt gatgtcgtag      1140
W--> 273 tataagcgcc ggtantkgaa ycaatatga cttttttaat gtgtgatgcc ttaagatggg      1200
W--> 275 tctttaatcc atgttaagnt tttgttaaag aaatagataa gtcttttaca agtatttgga      1260
W--> 277 tttactcaat gaaaaagagt canaaaatgt tcaactctc tccaaacata cactgaagaa      1320
W--> 279 agcataaaaa ttannaaata tattagaaca cgtatgtcca gtagcaawca maaattattg      1380
281 agtgttgayt gtgtctctac agatgggaaa ctgaggcaca cmaaagtac atttgtccga      1440
283 ggtaagattg ctagtaggta atgggggttg aattctaggg tcttaaccac caaaaatct      1500
285 gcatttttat tggcatttca attttttaa tatgttttta ctttaaaaaat caagttaaat      1560
287 acttaacttt ttaaaatcaa aatttgaaga aataatttga agattcagtg gattttcttt      1620
289 tttaaatctc tgagaaatct ctccctyca acgtgacacc maaaccmgag aaccagacag      1680
291 tttttcataa aatcatgaaa catgcyccmc maaaaataac ccactasca actgtgggac      1740
293 agattttgcc tcacatcatt gaaaaggcca gcawtcttt tctctctttc tttctttgkt      1800
295 gttttttttt tttcctgtag awacagggtc togtctgtg acccaggctg gtctyaaact      1860
297 cctggcctca agcgtacctc ctgcctctgc cttccaaagc actggaatta caagtgtgag      1920
299 ccgctgcaac ccgccagaaa aaagtgtgcc tttcatggcc ctgtctgggt ggctagacac      1980
301 gtgtgtgtgc tgggtgtcct gggccagcca gagttccctg agaggagcat gcatggccta      2040
303 aggaagttag cttcagggaa cagtgtatgac catcatttca cactcggacc cctgccmaa      2100
W--> 305 gatgggtgga tgsctgscag ggagggatcc cgggtktcct gcgcctggag aancctgcc      2160
W--> 307 aagcggaacc tgaaagtatn ccctgtcctt ttcttctcct nagataaagg ataggttaca      2220
W--> 309 gtttnggggtg ctcttgctgc gggaagacgt cgtcctgggg aggcctatga cccccaccna      2280
311 gataggccca agcctgctgc ctatcatgtg gcagctctac cctgatggac gataccgac      2340
313 ctcagactcc agtttctggc gcttagtgta ccacatcaag gtgagtgtct ttctcccaga      2400
315 ggtccatcgg ktgatcttgg gtttccctc cyematgtct gsccttagtg gtttaycttc      2460
W--> 317 ccycatccc agtssgcaa agcattwaaa aratggggga nrtrwacmas tgcagatttc      2520
W--> 319 tanaggactt taccagagag aaganagatc ctntgagggt tctaanagaa ccctacctcc      2580
W--> 321 acttctctcc anccaccanc taaccgcagg aagacatctc tgggtggggm kcacaggctg      2640
323 aaggctggtg ggaggaggr caktctccaa gasccctga aatcctcaca cctgggttcc      2700
325 tacctgctgt ttccagctag ggaagsgsc aggagttagg aatggaggga gtggagggtc      2760

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001

TIME: 15:22:26

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

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327 ctggccgata aatgccttct ctctctctct gcctctcaga ttgacggcgt ggaggacatg 2820
329 cttctcgagc tgctgccaga tgactgatgt atggtgagct ccaactggagc ctgacccctc 2880
331 ttagtccaca gtggctgtat cagaaagaaa gaccaccctt tctccatgaa ggcagtgcta 2940
333 acccctcccc gactgctgcc atctgagggg ccctagggat gggagaggct tcctggaggc 3000
335 actcatgtct cccttaccac ttccggagcc aagggtcttg gtaggcagcc ccctttatcg 3060
337 cagctgctca tatctataaa gtacttcaca agtttcagct ggcactttca ttttaccatt 3120
339 gctttttttt tctttgggag atgagtctgg ctctgtggcc caggctagag tgtagtgggt 3180
341 gcaatctcag ctcaactgaaa gctctgcctc ccgggttcac accattctcc tgccctcagcc 3240
343 ctccggagtag ctgggactac aggcgcgccgc caccacacct ggctaatttt tttttttttw 3300
345 ttwtwttttt tagtagagmc ggggtttcac cgtgttagcc aggatgggtc cgatctcctg 3360
347 acctcatgat ctgcccgcct cggcctccca aagtgcctgg attacaggca tgagccacca 3420
349 cgtccggcct taccattgct ttattaaata agcactgggt cttgattata tcagctgagc 3480
351 cagatattag atacgctatt gaggtttgrg gaaataagag taccaaaact cagaaatgag 3540
353 ttgaagtata gtgacatctt cagattacag acccagggtg cagaatttgc cttggctcag 3600
355 aaggcctctg ggggccatcc ctgaccacta ggcttccac ttagacctgc tccagcagca 3660
357 ccacccctcg scactgcctg gtcctttcct tcacccttga ttctgtcttc ttttgtcctt 3720
359 ctccaggctc tggyagcacc tgtctccttt caccacaggg cctgagcctg gccagcctac 3780
361 aatgggggat ttgtgtttct gttcaccttc gtttactatg bctgtgtctt ctccaccacg 3840
363 ctgggggtctg ggaggaatgg acagacagag gatgagctct acccrggggc tgsaggacct 3900
W--> 365 gtccctgtagm ccactctgct cgccttagsa cctacsactc cwrccgasga ggatnccant 3960
W--> 367 tggaagagct tcttnnaggt gncnaanaan anctgtgcgt nggcttttct cagctggatg 4020
W--> 369 atggtcntna gcctctttct gtcccttctg tccctcacag cactagtatt tnatgttgca 4080
371 caccactca gctccgtgaa tttgtgagaa cacaaccgat tcacctgagc aggacctctg 4140
W--> 373 aaacctgga ccagtggctc cacatgggtg tacgcctgca tgtaaacacg cctncaaacg 4200
375 ctgcctgccc gtraaacacgm sksyrmacag stgmswrocc gtaaacacgc ctgcaaacgc 4260
377 tgccctgccc cacagggttca cgtgcagctc aaggaaagrm ctgaaarrag cccttatctg 4320
W--> 379 tgctcaggac tcagaagcct ctgggtcagt ggtccacatc ccgggacgca gnaggaggcc 4380
381 aggccggcga gccctgtgga tgagccctca gaacccttgg gttgccacg tggaaaagg 4440
383 atagagggtt ggtttcccc cttttataga tggtcacgca cctgggtgtt acaaagttgt 4500
W--> 385 atgtggcatg aatacttgnt gtnatgattg attaaatgca agatagttaa tctaacttcg 4560
W--> 387 tgcggaatca gttctatcc ttgncttaga ttctgggtga gagaagtgan aataggcagn 4620
W--> 389 cccanataa anaatttca ngggatttat tttattnttc cttttggngn atnngggact 4680
W--> 391 acattntnnc nccccgtnta atccaatgnt taaancccca gtgttcttgg agnncntacg 4740
W--> 393 tcgaanacca ttggngtang caacctcaaa attttntngt tgnnaattnc cngttttcca 4800
W--> 395 gagnccccc cntnctccat cttnttctcn gccnccctn ncctccnca ntccnangt 4860
W--> 397 tnccctcgnc ccagtcagt tctttctecn nctttanccg ntatntcac cagnttcttt 4920
399 ct 4922

```

402 &lt;210&gt; SEQ ID NO: 6

403 &lt;211&gt; LENGTH: 20

404 &lt;212&gt; TYPE: DNA

OK 405 &lt;213&gt; ORGANISM: Artificial

407 &lt;220&gt; FEATURE:

408 &lt;223&gt; OTHER INFORMATION: p9A primer

410 &lt;400&gt; SEQUENCE: 6

411 tgctgccaga tgactgatgt

20

414 &lt;210&gt; SEQ ID NO: 7

415 &lt;211&gt; LENGTH: 20

416 &lt;212&gt; TYPE: DNA

OK 417 &lt;213&gt; ORGANISM: Artificial

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

fye →

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001

TIME: 15:22:27

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

L:19 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1  
L:97 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:99 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:99 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:136 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:166 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:203 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:405 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:417 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:429 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:441 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:453 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:465 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
L:477 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

RECEIVED

NOV 13 2001

TECH CENTER 1600/2900

## Raw Sequence Listing Error Summary

ERROR DETECTEDSUGGESTED CORRECTIONSERIAL NUMBER: 09/441,242

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s) 2 missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001

TIME: 15:22:26

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

PP. 215  
Does Not Comply  
Corrected Diskette Needed

6. Letters to

3 <110> APPLICANT: Russo, Giandomenico et al.  
 5 <120> TITLE OF INVENTION: TCL-1 Gene and Protein and Related Methods and Compositions  
 7 <130> FILE REFERENCE: 8666-008  
 9 <140> CURRENT APPLICATION NUMBER: 09/441,242  
 10 <141> CURRENT FILING DATE: 1999-11-16  
 12 <160> NUMBER OF SEQ ID NOS: 12  
 14 <170> SOFTWARE: PatentIn version 3.0  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 1324  
 18 <212> TYPE: DNA  
 C--> 19 <213> ORGANISM: Artificial  
 21 <220> FEATURE:  
 22 <223> OTHER INFORMATION: cDNA sequence of TCL-1  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (49)..(387)  
 28 <400> SEQUENCE: 1  
 29 cttgagagggc tctggtcttt gcttcttagg cggcccgagg acgccatg gcc gag tgc 57  
 30 Ala Glu Cys  
 31 1  
 33 ccg aca ctc ggg gag gca gtc acc gac cac ccg gac cgc ctg tgg gcc 105  
 34 Pro Thr Leu Gly Glu Ala Val Thr Asp His Pro Asp Arg Leu Trp Ala  
 35 5 10 15  
 37 tgg gag aag ttc gtg tat ttg gac gag aag cag cac gcc tgg ctg ccc 153  
 38 Trp Glu Lys Phe Val Tyr Leu Asp Glu Lys Gln His Ala Trp Leu Pro  
 39 20 25 30 35  
 41 tta acc atc gag ata aag gat agg tta cag tta cgg gtg ctc ttg cgt 201  
 42 Leu Thr Ile Glu Ile Lys Asp Arg Leu Gln Leu Arg Val Leu Leu Arg  
 43 40 45 50  
 45 cgg gaa gac gtc gtc ctg ggg agg cct atg acc ccc acc cag ata ggc 249  
 46 Arg Glu Asp Val Val Leu Gly Arg Pro Met Thr Pro Thr Gln Ile Gly  
 47 55 60 65  
 49 cca agc ctg ctg cct atc atg tgg cag ctc tac cct gat gga cga tac 297  
 50 Pro Ser Leu Leu Pro Ile Met Trp Gln Leu Tyr Pro Asp Gly Arg Tyr  
 51 70 75 80  
 53 cga tcc tca gac tcc agt ttc tgg cgc tta gtg tac cac atc aag att 345  
 54 Arg Ser Ser Asp Ser Ser Phe Trp Arg Leu Val Tyr His Ile Lys Ile  
 55 85 90 95  
 57 gac ggc gtg gag gac atg ctt ctc gag ctg ctg cca gat gac 387  
 58 Asp Gly Val Glu Asp Met Leu Leu Glu Leu Leu Pro Asp Asp  
 59 100 105 110  
 61 tgatgtatgg tcttggcagc acctgtctcc tttcacccca gggcctgagc ctggccagcc 447  
 63 tacaatgggg atgttgtgtt tctgttcacc ttcgtttact atgcctgtgt cttctccacc 507  
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 69 ttggcagagc ttcttcagg tgccageta tacctgtgcc tcggttttc tcagctggat 687  
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/441,242

DATE: 07/26/2001

TIME: 15:22:26

Input Set : A:\8666-008seqlist.txt

Output Set: N:\CRF3\07262001\I441242.raw

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87 tgtggcatga atactttttg taatgattga ttaaagcaa gatagtttat ctaacttcgt 1227
89 gcgcaatcag cttctatcct tgacttagat tctggtggag agaagtgaga ataggcagcc 1287
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96 <212> TYPE: PRT
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W--> 99 <223> OTHER INFORMATION:
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106 20 25 30
109 Trp Leu Pro Leu Thr Ile Glu Ile Lys Asp Arg Leu Gln Leu Arg Val
110 35 40 45
113 Leu Leu Arg Arg Glu Asp Val Val Leu Gly Arg Pro Met Thr Pro Thr
114 50 55 60
117 Gln Ile Gly Pro Ser Leu Leu Pro Ile Met Trp Gln Leu Tyr Pro Asp
118 65 70 75 80
121 Gly Arg Tyr Arg Ser Ser Asp Ser Ser Phe Trp Arg Leu Val Tyr His
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125 Ile Lys Ile Asp Gly Val Glu Asp Met Leu Leu Glu Leu Leu Pro Asp
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129 Asp
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160 atggccgagt gcccgacact

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*see item 11 on Eva Summary Sheet*